Amendments to the Specification

Please replace the paragraph beginning on page 10, line 1 with the following amended paragraph:

FIGs. 2A-2D ~~FIG. 2.~~ Modifications in the nucleotide sequence of the p7.5/tk (SEQ ID NO:5) vaccinia transfer plasmid. Four new vectors, p7.5/ATG0/tk (SEQ ID NO:6), p7.5/ATG1/tk (SEQ ID NO:7), p7.5/ATG2/tk (SEQ ID NO:8) and p7.5/ATG3/tk (SEQ ID NO:9) have been derived as described in the text from the p7.5/tk vaccinia transfer plasmid. Each vector includes unique BamHI, SmaI, PstI, and SalI sites for cloning DNA inserts that employ either their own endogenous translation initiation site (in vector p7.5/ATG0/tk (SEQ ID NO:6)) or make use of a vector translation initiation site in any one of the three possible reading frames (p7.5/ATG1/tk (SEQ ID NO:7), p7.5/ATG2/tk (SEQ ID NO:8) and p7.5/ATG3/tk (SEQ ID NO:9)).

Please replace the paragraph beginning on page 11, line 15 with the following amended paragraph:

FIGs 8A and 8B ~~FIG. 8~~. Differential expression in tumor lines of differential display clone 90. RNase ~~Rnase~~ protection assay: 300 picograms of clone 90 antisense probe was hybridized with 5 micrograms total RNA prior to RNase digestion and analysis of protected fragments on 5% denaturing PAGE.

Please replace the paragraph beginning on page 12, line 7 with the following amended paragraph:

FIGs 11A and 11B ~~FIG. 11~~. Southern Blot Analysis of Viral Genomes p7.5/tk (FIG. 11A) and pEL/tk (FIG. 11B). The viruses v7.5/tk and vEL/tk were used to infect a well of a 6 well dish of BSC-1 cells at high multiplicity of infection (moi) and after 48 hours the cells were harvested and the DNA was isolated using DNAzol (Gibco). The final DNA product was resuspended in 50 microliters of TE 8.0 and 2.5 microliters were digested with HindIII, HindIII and ApaI, or HindIII and Not I, electrophoresed through a 1.0% agarose gel, and transferred to Nytran (Schleicher and Schuell) using a Turboblotter (Schleicher and Schuell). The samples were probed with p7.k/tk (FIG 11A [[a]]) or pEL/tk (FIG. 11B [[b]]) labeled with ^{32}P using Random Primer DNA Labeling Kit (Bio-Rad) in QuickHyb (Stratagene). The lower portion of the figure denotes a map of the HindIII J fragment with the positions of the HindIII, NotI, and ApaI sites illustrated. The leftmost 0.5 kilobase fragment has electrophoresed off the bottom of the gel.

Please replace the paragraph beginning on page 65, line 11 with the following amended paragraph:

In preliminary experiments, an average of three differentially displayed bands were identified for each pair of primers. With a total of 66 primer pairs generated from all possible combinations of 12 independent primers, approximately 200 gene fragments could be identified. In some cases multiple fragments may derive from the same gene. FIG. 7 shows the pattern of differential display fragments observed with one pair of arbitrary decamers, MR_1 (TAC AAC GAG G) (SEQ ID NO:11) and MR_5 (GGA CCA AGT C)

(SEQ ID NO:13). A number of bands can be identified that are associated with all four tumors but not with the parental cells. This distribution is unrelated to the immunogenicity of the tumor cells, since only three of the four tumors are immunologically crossreactive. In contrast to the differentially expressed bands identified by RDA, which gave positive results on the Northern blots exposed for only a few hours, fragments identified by differential display did not give a signal on Northern blots even after several days. Differential expression of the differential display fragments can, however, be confirmed by RNase protection assays or by semi-quantitative PCR with sequence specific primers. An example is shown in FIGs. 8A and 8B ~~FIG. 8~~ the results of an RNase protection assay with clone 90 from differential display band 9. This sequence, which has no significant homology to entries in the GenBank database, is expressed in all four tumor lines but not in the parental B/c.N.

Please replace the paragraph beginning on page 79, line 13 with the following amended paragraph:

One well of a 6 well dish of BSC-1 was infected with v7.5/tk or vEL/tk at high multiplicity of infection (moi) and after 48 hours the cells were harvested, pelleted by low speed centrifugation, rinsed with Phosphate-Buffered Saline (PBS), and the DNA was isolated using DNAzol (Gibco). The final DNA product was resuspended in 50 microliters of TE (10mM TrisHCl, pH 8.0~~,~~ 1 mM EDTA) and 2.5 microliters were digested with HindIII, HindIII and ApaI, or HindIII and NotI, electrophoresed through a 1.0% agarose gel, and transferred to Nytran (Schleicher and Schuell) using a Turboblotter (Schleicher and Schuell). The samples were probed with p7.5/tk (FIG. 11A[[a]]) or pEL/tk (FIG. 11B[[b]])

labeled with ^{32}P using Random Primer DNA Labeling Kit (Bio-Rad) in QuickHyb (Stratagene) and visualized on Kodak XAR film.

Please replace the paragraph beginning on page 84, line 7 with the following amended paragraph:

The genomes for vEL/tk and v7.5/tk were analyzed by Southern blotting to confirm the location of the ApaI and NotI sites in the HindIII J fragment as shown in FIGs. 11A and 11B ~~FIG. 11~~. The filters were hybridized to ^{32}P labeled HindIII J fragment derived from the p7.5/tk or pEL/tk. The genomes for v7.5/tk and vEL/tk have an ApaI site that does not appear in vNotI/tk (compare lanes 7 and 8 to lane 5 in each blot) whereas digestion with NotI and HindIII yield a set of fragments of equivalent size. The 0.5 kilobase HindIII/NotI or HindIII/ApaI fragment from the left hand side of HindIII J produced from NotI or ApaI digestion has electrophoresed off the bottom of the agarose gel.

Please replace the Abstract page with the attached amended Abstract page.

Amendments to the Drawings

Please replace the original drawings with the attached drawings. Figure 2 has been relabeled as Figures 2A-2D.